

```

1 MPARRLLLLTLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||
1 MPARRLLLLTLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50

51 SIKWTLKEDPVLQVPTHVEEPAFLPDNDGSLYTLGSKNNEGLTKLPFTI 100
  |||
51 SIKWTLKEDPVLQVPTHVEEPAFLPDNDGSLYTLGSKNNEGLTKLPFTI 100

101 PELVQASPCRSSDGILYMGGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150
  |||
101 PELVQASPCRSSDGILYMGGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150

151 TSLLYLGRTEYTIITMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200
  |||
151 TSLLYLGRTEYTIITMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200

201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250
  |||
201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250

```

FIG. 1

```

251 RYLTFFMSGVGRITKKWKYPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
|||||
251 RYLTFFMSGVGRITKKWKYPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300

301 HEGVAVVPRGSTLPLLEGPTDGVITIGDKGECVITPSTDVKFDPGLKSKN 350
|||||
301 HEGVAVVPRGSTLPLLEGPTDGVITIGDKGECVITPSTDVKFDPGLKSKN 350

351 KLNLYLRNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKSF 400
|||||
351 KLNLYLRNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKSF 400

401 EE..TLLQMTS 409
|| :|::||
401 EEVINLVDQTS 411

```

FIG. 1 (CONT.¹)

```

5  QLQSVSSAIHLCDKMKMELSLNIPVNHGPQEESCGSSQLHENSGBPETS 54
   :|||||||||||||||||||||||||||||||||||||||||||||
313 KLQSVSSAIHLCDKMKMELSLNIPVNHGPQEESCGSSQLHENSGBPETS 362

   . . . . .
55  SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSHWDSTISGSQRAAFCDHKT 104
   |||||||||||||||||||||||||||||||||||||||||||
363 SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSHWDSTISGSQRAAFCDHKT 412

   . . . . .
105 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTACLNQSLDA 154
   |||||||||||||||||||||||||||||||||||||||||||
413 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTACLNQSLDA 462

   . . . . .
155 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVI VQKLKDN 204
   |||||||||||||||||||||||||||||||||||||||||||
463 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVI VQKLKDN 512

   .
205 KQMG LQPYPEILVVSRSRPSLNLLQNKSM 232
   |||||||||||||||||||||||||||||||
513 KQMG LQPYPEILVVSRSRPSLNLLQNKSM 540

```

FIG. 2

FIG. 3

```

1  MGLVSSKKPDKEKPIKEKDKGQWSPLKVSQDKDAPPLPPLVFNHLLTPP 50
   |||||
1  MGLVSSKKPDKEKPIKEKDKGQWSPLKVSQDKDAPPLPPLVFNHLLTPP 50

51 PPDEHLDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSL 100
   |||||
51 PPDEHLDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSL 100

101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
   |||||
101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150

151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYISPRITFPSLQA 200
   |||||
151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYISPRITFPSLQA 200

201 LVQHYS..... 206
     |||||

201 LVQHYSKKGDLGCQRLTLPCVRPAPQNPWAQDEWEIPRQSLRLVRKLGSG 250

207 .....SYKNNMKVAIKTLKEGTMSPAEFLGEANVMKALQHERLVRLY 249
     :|||||
251 QFGEVWMGYKNNMKVAIKTLKEGTMSPAEFLGEANVMKALQHERLVRLY 300

```

FIG. 4

```
.      .      .      .      .  
250 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAY   299  
.      |      |      |      |      |      |      |      |      |  
    |||||      |      |      |      |      |      |      |      |  
301 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAY   350  
  
    .      .      .      .      .  
300 IERMNSIHRDLRAANILVSEALCCKIADFGGLARIIDSEYTAQEGAKFFPIK   349  
    |||||      |      |      |      |      |      |      |      |  
351 IERMNSIHRDLRAANILVSEALCCKIADFGGLARIIDSEYTAQEGAKFFPIK   400  
  
    .      .      .      .      .  
350 WTAPEAIHFGVFTIKADVWSFVGVLMEVVTYGRVPYPGMSNPEVIRNLER   399  
    |||||      |      |      |      |      |      |      |      |  
401 WTAPEAYHFGVFTIKADVWSFVGVLMEVVTYGRVPYPGMSNPEVIRNLER   450  
  
    .      .      .      .      .  
400 GYRMPRPDTCPPELYRGVIAECWRSRPERPTFEFLQSLEDFYTATERQ     449  
    |||||      |      |      |      |      |      |      |      |  
451 GYRMPRPDTCPPELYRGVIAECWRSRPERPTFEFLQSLEDFYTATERQ     500
```

```
         450 YELQP 454  
           |||||  
        501 YELQP 505
```

FIG. 4 (CONT.)

```

1  MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIR 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIR 50

```

FIG. 5

FIG. 6

1 VFLGRCSVKEFEKLNRI GEGTYGIVRARDTQTDEI VALKKVRMDKEKD 50
 |||||
 1 VFLGRCSVKEFEKLNRI GEGTYGIVRARDTQTDEI VALKKVRMDKEKD 50
 |||||
 51 GIPISSLREITLLRLRHPNIVELKEVVVGNHLESIFLVMGYCEQDLASL 100
 |||||
 51 GIPISSLREITLLRLRHPNIVELKEVVVGNHLESIFLVMGYCEQDLASL 100
 |||||
 101 LENMPTPFSEAQVKCIVLQVLRGLQYLHRNFI IHRDLKVSNLLMTDKGCV 150
 |||||
 101 LENMPTPFSEAQVKCIVLQVLRGLQYLHRNFI IHRDLKVSNLLMTDKGCV 150
 |||||
 151 KTGGCNLGQAWSL 163
 ||: :|::|:::
 151 KTADFGLARAYGV 163

FIG. 7

```

22  AVGCILAE1LLAHR2PL3LP4GTSE5IHQ6IDL7IVQ8LLGTP9SENI10WPG11FSKL12PL13VG 71
    |||||14|||||15|||||16|||||17|||||18|||||19|||||20|||||21|||||22|||||23
197 AVGCILAE24LLAHR25PL26LP27GTSE28IHQ29IDL30IVQ31LLGTP32SENI33WPG34FSKL35PL36VG 246
    |||||37|||||38|||||39|||||40|||||41|||||42|||||43|||||44|||||45
72  QYSLRKQ46PYNN47LKH48KFP49WLSE50AGL51RL52LHF53LFMY54DP55KK56RAT57AGDC58LESS59YF 121
    |||||60|||||61|||||62|||||63|||||64|||||65|||||66|||||67|||||68|||||69
247 QYSLRKQ70PYNN71LKH72KFP73WLSE74AGL75RL76LHF77LFMY78DP79KK80RAT81AGDC82LESS83YF 296
    |||||84|||||85|||||86|||||87|||||88|||||89|||||90|||||91|||||92|||||93
122 KEKPLRL94PISG95VCEG96CREPG 141
    |||||97|||||98|||||99|||||100|||||101|||||102|||||103
297 KEKPLRL104PISG105VCEG106CREPG 316

```

FIG. 8

```
1 VFLGRCSVKEFEKLNRI GEGTYGIVYRARDTQTDEI VALKKVRMDKEK 50
  |||||
1 VFLGRCSVKEFEKLNRI GEGTYGIVYRARDTQTDEI VALKKVRMDKEK 50

      .
51 GIPSSLREITLLRLRHPNIV 72
   |||||
51 GIPSSLREITLLRLRHPNIV 72
```

FIG. 9

```

1  MGEAEKFHYIYSCDL DINVQLKIGSLEGRQKSYKAVLEDPMLKFSGLY 50
  |||||
1  MGEAEKFHYIYSCDL DINVQLKIGSLEGRQKSYNAVLEDPMLKFSGLY 50
  |||||
51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
  |||||
51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
  |||||
101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMFRQGMHDLKVWP NVE 150
  |||||
101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMSRQGMHDLKVWP NVE 150
  |||||
151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLTKAHRQGHMV KVDWLDRLTFRE 200
  |||||:|||||
151 ADGSEPTNTPGRTSS TLSEDQMSRLAKLTKAHRQGHMV KVDWLDRLTFRE 200
  |||||
201 IEMINESVKRSSNFMYL MGGFRCVKCDDKEYGIVVYEKDGDESSPILTSF 250
  |||||
201 IEMINESVKRSSNFMYL MGGFRCVKCDDKEYGIVVYEKDGDESSPILTSF 250
  |||||
251 ELVKVPDPQMSLENL VESKHHNLPRLSRGPSDHD LKPYSPRDQLKNIV 300
  |||||
251 ELVKVPDPQMSLENL VESKHHNLPRLSRGPSDHD LKPYSPRDQLKNIV 300
  |||||

```

FIG. 10

301	SYPPSKPPTYEEQDLVWEFFRYL	TNQDKALTKILT	SVIWDLPQEAKQALA	350
301	SYPPSKPPTYEEQDLVWEFFRYL	TNQDKALTKILT	SVIWDLPQGAKQALA	350
351	LLGKNPMDVEDSLEL	ISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV	400	
351	LLGKNPMDVEDSLEL	ISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV	400	
401	QALKYENFDDIKNGLEPTKKDSQSSV	SENSGINSAEIDSSQIITSPL	450	
401	QALKYENFDDIKNGLEPTKKDSQSSV	SENSGINSAEIDSSQIITSPL	450	
451	PSVSSPPASKTKEVPDGENLEQDLCTFL	ISRACKNSTLANYLYWYVIVE	500	
451	PSVSSPPASKTKEVPDGENLEQDLCTFL	ISRACKNSTLANYLYWYVIVE	500	
501	CEDQDTQQRDPKTHEMYLNV	MRRFSQALLKGDKSVRVMRSL	AAQQTFVD 550	
501	CEDQDTQQRDPKTHEMYLNV	MRRFSQALLKGDKSVRVMRSL	AAQQTFVD 550	

FIG. 10 (CONT.)¹

FIG. 10 (CONT.)²

1 MGEAEKFHYIYSCDLINVLKIGSLEKREQKSYKAVLEDPMLKFSGLY 50
 |||||
 1 MGEAEKFHYIYSCDLINVLKIGSLEKREQKSYNAVLEDPMLKFSGLY 50
 |||||
 51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNNEWLKLVPKYPD 100
 |||||
 51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNNEWLKLVPKYPD 100
 |||||
 101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMFRQGMHDLKVWP 150
 |||||
 101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMSRQGMHDLKVWP 150
 |||||
 151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTF 200
 |||||
 151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTF 200
 |||||
 201 IEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSF 250
 |||||
 201 IEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSF 250
 |||||
 251 ELVKVPDPQMSLENLVESKHHNLPRLSRGPSDHD LKPYSPRDQLKNIV 300
 |||||
 251 ELVKVPDPQMSLENLVESKHHNLPRLSRGPSDHD LKPYSPRDQLKNIV 300

FIG. 11

501 FC 502
500 EC 501

FIG. 11 (CONT.¹)


```

1  MGNAAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
   |||||
1  MGNAAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
   |||||

51  GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
   |||||
51  GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
   |||||

101  FPFLVKLEFSFKDNSNLYMVMEYVPGGEMFSHLRRIGRF 139
    |||||
101  FPFLVKLEFSFKDNSNLYMVMEYVPGGEMFSHLRRIGRF 139
    |||||

```

FIG. 12

```

1  MVVFNGLLKIKICEAVSLKPTAWSLRHAVGPRPQTFLLDPYIALNVDDSR 50
   |||||
1  MVVFNGLLKIKICEAVSLKPTAWSLRHAVGPRPQTFLLDPYIALNVDDSR 50
   . . .
51 IGQTATKQKTNSPAWHDEFVTDVCNGRKKIELAVFHDAPIGYDDFVANCTI 100
   |||||
51 IGQTATKQKTNSPAWHDEFVTDVCNGRKKIELAVFHDAPIGYDDFVANCTI 100
   . . .
101 QFEELLQNGSRHFEDWIDLEPEGRVYVIIDLSSGSEVKIPNSAFCEER 150
   |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVIIDLSSGSEAPKDNEERVFRER 150
   151 VEMR 154
   :: |
   151 MRPR 154

```

FIG. 13

FIG. 14

FIG. 14 (CONT.)¹

FIG. 15

```

21 KSGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 70
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
295 EKGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 344

71 GGSVIKYSKNTTRKQWLKETPDTLLNILKNADLSLAFQTYTYIRPGSEGF 120
   |::::::::::::::::::::::::::::::::::::::::::::::::::::
345 GGSVIKYSKNTTRKQWLKETPDTLLNILKNADLSLAFQTYTYIRPGSEGF 394

121 LKGPLSEETEASDSVDGGHDSVILDPERLEPGLDEEDTDFFEEEDDNPDWV 170
   |::::::::::::::::::::::::::::::::::::::::::::::::::::
395 LKGPLSEETEASDSVDGGHDSVILDPERLEPGLDEEDTDFFEEEDDNPDWV 444

171 SELKKRAGWQGLCDR 185
   |::::::::::::::::
445 SELKKRAGWQGLCDR 459

```

FIG. 16

FIG. 17

```

1 MAESAGASSFFPLVLLLAGSGGPRGVQALLCACTSCIQANYTCETDG 50
  |||||
1 MAESAGASSFFPLVLLLAGSGGPRGVQALLCACTSCIQANYTCETDG 50

51 ACMVSIFNLDMGMEHHVRTCIPKVELVPAGKPFYCLSSDLRNTHCCYTDY 100
  |||||
51 ACMVSIFNLDMGMEHHVRTCIPKVELVPAGKPFYCLSSDLRNTHCCYTDY 100

101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGVPFLLFLIIIVFLVIN 150
  |||||
101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGVPFLLFLIIIVFLVIN 150

151 YHQRVYHNQRQRLDMEDPSCMCLSKDKTLQDLVYDLSTSGSGSGTKFF 198
  |||||
151 YHQRVYHNQRQRLDMEDPSCMCLSKDKTLQDLVYDLSTSGSGSGGLPLF 198

```

FIG. 18

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
|||||
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
51 HNGERRIIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100
|||||
51 HNGERRIIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100
101 DKAIDILDRSSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQSAGD 150
|||||
101 DKAIDILDRSSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQSAGD 150
151 INTIYQPEPRSRHLSVSSQNPGRSSPPGYVPERQQHARQGSYTSINS 200
|||||
151 INTIYQPEPRSRHLSVSSQNPGRSSPPGYVPERQQHARQGSYTSINS 200
201 EGEFIPETSEQCMLDPLSSAENSLGSCQSLDRSADSPSFRKSRMSRAQS 250
|||||
201 EGEFIPETSEQCMLDPLSSAENSLGSCQSLDRSADSPSFRKSRMSRAQS 250

FIG. 19

```

251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFPRIRR 300
|||||
251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFPRIRR 300

301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRILRSADSENALSVQERN 350
|||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRILRSADSENALSVQERN 350

351 VPTKCEELSLARRRLPRWSQTSYGGKQLG 379
|||| : ||
351 VPTKSPSAPINWRR.....GKLLG 369

```

FIG. 19 (CONT.¹)

FIG. 20

FIG. 20

```

251 AENSLGSCQSLDRSADSPFRKSRMSRAQSPFDNRQEYSDRETQLYDKG 300
    |||||
220 AENSLGSCQSLDRSADSPFRKSRMSRAQSPFDNRQEYSDRETQLYDKG 269
    . . . . .
301 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 350
    |||||
270 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 319
    . . . . .
351 ENMGLAVQYLDPRGRLRSADSENALSVOERNVPTKCEELSLARRRLPRWS 400
    |||||
320 ENMGLAVQYLDPRGRLRSADSENALSVOERNVPTKSPAPINWRR..... 364
    .
    401 QTSYGGKQLG 410
        || ||
    365 ..... GKLLG 369

```

FIG. 20 (CONT.¹)

[illegible]

FIG. 21

FIG. 21 (CONT.¹)

FIG. 22

1 MATSRYEPVAEIGVGAYGTVVKARDPHSGHFCALKSVRVP 40
| | | | | | | | | | | | | | | | | | | | | |
1 MATSRYEPVAEIGVGAYGTVVKARDPHSGHFVALKSVRVP 40

FIG. 23


```

34 PLPLEPRAVYCKDVL DIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPWQN 83
   |: :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
464 PEVPDPRAVYCKDVL DIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPWQN 513
      .
84 EMIETECFKELNVFGPNGLTPPDLNRNHPPEPPKKGLLQRLFKRQHQNNS 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
514 EMIETECFKELNVFGPNGLTPPDLNRNHPPEPPKKGLLQRLFKRQHQNNS 563
      .
      134 KSSPSSKTSFNHHHINSNHVSSNSTGSS 160
         |||:|||||:|||||:|||||:|||||:|||||:|||||
      564 KSSPSSKTSFNHHHINSNHVSSNSTGSS 590

```

FIG. 24

```

28  LLSPSGHIRISDLGLAVKIPEGLIRGRVGTGYMAPEVLNNQRYGLSPD 77
   ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LLDDYGHIRISDLGLAVKIPEGLIRGRVGTGYMAPEVLNNQRYGLSPD 367

   . . . . .
78  YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEAK 127
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
368 YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEAK 417

   . . . . .
128 SICKMLLTAKQRLGCQEEGAAEVKRHPFFRNMNFKRLEAGMLDPPFVP 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 SICKMLLTAKQRLGCQEEGAAEVKRHPFFRNMNFKRLEAGMLDPPFVP 467

   . . . . .
178 DPRVYCKDVL DIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPWQNE MIE 227
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 DPRVYCKDVL DIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPWQNE MIE 517

   . . . . .
228 TECFKELNVFGPNGTLPDLNRNHPPEPPKKGLLQRLFKRQHQNNSKSSP 277
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
518 TECFKELNVFGPNGTLPDLNRNHPPEPPKKGLLQRLFKRQHQNNSKSSP 567

   . . . . .
278 SSKTSFNHHHINSNHVSSNSTGSS 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
568 SSKTSFNHHHINSNHVSSNSTGSS 590

```

FIG. 25

FIG. 26

```

1  MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
  |||||
1  MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
  |||||
51  MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPVEVTVGVSVLAERCKKNNG 100
  |||||
51  MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPVEVTVGVSVLAERCKKNNG 100
  |||||
101  KAEFWLDLQPQAKVLM SVQYFLEDVDCKQSMRSEDEAKFPTMNRRAIKQ 150
  |||||
101  KAEFWLDLQPQAKVLM SVQYFLEDVDCKQSMRSEDEAKFPTMNRRAIKQ 150
  |||||
151  AKIHIKNHEFIATFFGQPTFCSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
  |||||
151  AKIHIKNHEFIATFFGQPTFCSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
  |||||
201  IDKIIGRCTGTAANSRDTIFQKERFNIDMPHRFKVHNYMSPTFCDHCGSL 250
  |||||
201  IDKIIGRCTGTAANSRDTIFQKERFNIDMPHRFKVHNYMSPTFCDHCGSL 250
  |||||
251  LLPAPHDKHQW.....DCG 264
  |
251  L.....WGLVKQGLKCEDCG 265
  |

```

FIG. 27

1 MDETHPGYGKEVDLEFLVSPSLPCLLSFAGSARHLVPPDSNLFSKLWACG 50
|||||
203 MDETHPGYGKEVD.....LWACG 220
51 VILFTLLAGSPFWHRRQILMLRMIMEGQYQFSSPEWDDRSSTVKDLISR 100
|||||
221 VILFTLLAGSPFWHRRQILMLRMIMEGQYQFSSPEWDDRSSTVKDLISR 270
101 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 150
|||||
271 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 320
151 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKGEQQNR 200
|||||
321 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKGEQQNR 370
201 AALFQHRPPGPPFIMGPEEEGDSAAITDEAVLVLG 236
|||||
371 AALFQHRPPGPPFIMGPEEEGDSAAITDEAVLVLG 406

FIG. 28

1 MAFCAKMRSSKKTEVNLEAPEPGVEVIFYLSDRPLRLGSGEYTAEEELCI 50
 |||||
 1 MAFCAKMRSSKKTEVNLEAPEPGVEVIFYLSDRPLRLGSGEYTAEEELCI 50
 |||||
 51 RAAQACRISPLCHNLFALYDENTKWLWYAPNRTITVDDKMSRLHRYMRFY 100
 |||||
 51 RAAQACRISPLCHNLFALYDENTKWLWYAPNRTITVDDKMSRLHRYMRFY 100
 |||||
 101 FTNWHTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
 |||||
 101 FTNWHTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
 |||||
 151 QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAI SHYAMMKMQLPELP 200
 |||||
 151 QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAI SHYAMMKMQLPELP 200
 |||||
 201 KDISYKRYIPETLNKSIRQRNLLTRMRINN VFKDFLKEFNNTKICDSSVS 250
 |||||
 201 KDISYKRYIPETLNKSIRQRNLLTRMRINN VFKDFLKEFNNTKICDSSVS 250
 |||||
 251 THDLKVKYLATLET LTKHYGAEI FETSMLLISSENEMNWFHSDNGGNVLY 300
 |||||
 251 THDLKVKYLATLET LTKHYGAEI FETSMLLISSENEMNWFHSDNGGNVLY 300
 |||||

FIG. 29

FIG. 29 (CONT.¹)

[illegible]

FIG. 30


```

1  MGCVQCKDKEATKLTEERDGSLNQSSGYRYGTDPTPQHYPSTGVTIPNY 50
  |||||
1  MGCVQCKDKEATKLTEERDGSLNQSSGYRYGTDPTPQHYPSTGVTIPNY 50
  .
51 NNFHAAGGQGLTVFGGVNSSHTGLRTRGGTGVTLFVALYDYEARTEDD 100
  |||||
51 NNFHAAGGQGLTVFGGVNSSHTGLRTRGGTGVTLFVALYDYEARTEDD 100
  .
101 LSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVDSIQAEFWY 150
  |||||
101 LSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVDSIQAEFWY 150
  .
151 FGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAYSLSIRDWDDMKGDHV 200
  |||||
151 FGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAYSLSIRDWDDMKGDHV 200
  .
201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
  |||||
201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
  .

```

FIG. 31

251 PRLDLSVKT KD VWEI PRES LQLIKRLGNGQFGEVWMGTWNGNTKVAIKT 300
|||||
251 PRLDLSVKT KD VWEI PRES LQLIKRLGNGQFGEVWMGTWNGNTKVAIKT 300
301 LKPGTMSPE SFL EEAQIMKKLKHDKLVQLYAVVSEEP IYIVTEYMNKG 348
|||||
301 LKPGTMSPE SFL EEAQIMKKLKHDKLVQLYAVVSEEP IYIVTEYMNKG 348

FIG. 31 (CONT.¹)

```

50 S L E L H K R R K A L T E P E A R Y Y L R Q I V L G C Q Y L H R N R V I H R D L K L G N L F L N E      99
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
137 S L E L H K R R K A L T E P E A R Y Y L R Q I V L G C Q Y L H R N R V I H R D L K L G N L F L N E      186

100 D L E V K I G D F G L A T K V E Y D G E R K K T L C G T P N Y I A P E V L S K K G H S F E V D V W S      149
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
187 D L E V K I G D F G L A T K V E Y D G E R K K T L C G T P N Y I A P E V L S K K G H S F E V D V W S      236

150 I G C I M Y T L L V G K P P F E T S C L K E T Y L R I K K N E Y S I P K H I N P V A A S L I Q K M L      199
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
237 I G C I M Y T L L V G K P P F E T S C L K E T Y L R I K K N E Y S I P K H I N P V A A S L I Q K M L      286

200 Q T D P T A R P T I N E L L N D E F F T S G Y I P A R L P I T C L T I P P R F S I A P S S L D P S N      249
   | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
287 Q T D P T A R P T I N E L L G D E F F T S G Y I P A R L P I T C L T I P P R F S I A P S S L D P S N      336

250 R K P L T V L N K G L E N P L P E R P R E K E E P V V R E T G E V V D C H L S D M L Q Q L H S V N A      299
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
337 R K P L T V L N K G L E N P L P E R P R E K E E P V V R E T G E V V D C H L S D M L Q Q L H S V N A      386

```

FIG. 32

```

300 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSKYGLGYQLCDNSVGVLFF 349
|||||
387 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSKYGLGYQLCDNSVGVLFF 436
.
350 NDSTRILLYNDGDSLQYIERDGTESYLTVSSHPSNLMKKITLLKYFRNYM 399
|||||
437 NDSTRILLYNDGDSLQYIERDGTESYLTVSSHPSNLMKKITLLKYFRNYM 486
.
400 SEHLLKAGANITPREGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 449
|||||:|||||
487 SEHLLKAGGNITPRQGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 536
.
450 DHTKLILCPLMAAVTYIDEKRDFRTYRLSLLEEEYGCKKELASRLRYARTM 499
|||||
537 DHTKLILCPLMAAVTYIDEKRDFRTYRLSLLEEEYGCKKELASRLRYARTM 586
.
500 VDKLLSSRSASNRLKAS 516
|||||
587 VDKLLSSRSASNRLKAS 603
    
```

FIG. 32 (CONT.¹)

FIG. 33

```

32  ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
    |: :: ::||:  ||||| ||||| ||||| ||||| ||||| |||||
230 EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279
    .
    82  QGFSYDYVFDWNMLKFGASSSQAQPRD 108
        ||||| ||||| ||||| ||||| : | : |
    280 QGFSYDYVFDWNMLKFGAARN...PED 303

```

FIG. 34

FIG. 35

167 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPELPGGDDLKS 216
|||||
1 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPELPGGDDLKS 50
217 PEEKKTATQLHSKRRPK 233
|||||:|||||
51 PEEKKTTTQLHSKRRPK 67

FIG. 36

•

FIG. 37

FIG. 37 (CONT.)¹

```

1 MSAKVRLLKKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECSHSALRRDK 50
  |||
1 MSAKVRLLKKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECSHSALRRDK 50

. . . . .
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVIGRGAFGEVAVVKMKNTER 100
  |||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVIGRGAFGEVAVVKMKNTER 100

. . . . .
101 IYAMKILNKKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||
101 IYAMKILNKKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150

. . . . .
151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLDAIDSIHQLHYVHRD 200
  |||
151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLDAIDSIHQLHYVHRD 200

. . . . .
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231
  |||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231

```

FIG. 38

```

1 MELRVGNRYRLGRKIGSGSFGDIYL..... 25
  |||||
1 MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVTKHPQLH 50
  .
26 .....VGIP TIRWC GAEGDYNVMVMELLGPSLEDLNFCSRKF 63
  |||||
51 IESKIYKMMQGGVGIPTIRWC GAEGDYNVMVMELLGPSLEDLNFCSRKF 100
  .
64 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKGNLVYIIDF 113
  |||||
101 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKGNLVYIIDF 150
  .
114 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 163
  |||||
151 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 200
  .
164 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 213
  |||||
201 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 250

```

FIG. 39

[illegible]FIG. 39 (CONT.¹)

```

14 TFAAPSFDDKILEVVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 63
   |||||
817 TFAAPSFDDKILEVVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 866

   . . . . .
64 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEQKQKCEL 113
   |||||
867 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEQKQKCEV 916

   . . . . .
114 PRPPSCSLHPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMEQELA 163
   |||||
917 PRPPSCSLHPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMEQELA 966

   . . . . .
164 HAVNASSKSMDRVYGKPRTTTEGLNCSEFVLEMVNNFRALRSETELLSGKM 213
   |||||
967 HAVNASSKSMDRVYGKPRTTTEGLNCSEFVLEMVNNFRALRSETE.LLSGKM 1015

   . . . . .
214 ALQLDPPQKEQLGSALAEMDRQLRRIADTPWLCQSAEPGDEESVMLDLAK 263
   |||||
1016 ALQLDPPQKEQLGSALAEMDRQLRRIADTPWLCQSAEPGDEESVMLDLAK 1065

```

FIG. 40

364 AVEA 367

1166 AVEA 1169

FIG. 40 (CONT.¹)

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FIG. 41

FIG. 42

FIG. 42 (CONT.)¹

14	GEVDLTALAKELRAVEDVRPPHKVTDYSSSSSEESGTTDEEDDDVEQEGAD	63
674	GEVDLTALAKELRAVEDVRPPHKVTDYSSSSSEESGTTDEEDDDVEQEGAD	723
64	ESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPAMTPSKEGTLIV	113
724	ESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPAMTPSKEGTLIV	773
114	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	163
774	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	823
164	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	213
824	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	873
214	NLLVGTESGIMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLVTISGKKD	263
874	NLLVGTESGIMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLVTISGKKD	923
264	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	313
924	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	973

FIG. 43

314	VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLDLTVEEGQRLKVI	363
974	VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLDLTVEEGQRLKVI	1023
364	YGSCAGFHAVDVGSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY	413
1024	YGSCAGFHAVDVGSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY	1073
414	EDEGVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVE	463
1074	EDEGVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVE	1123
464	TGHLDGVMHKRAQRLKFLCERNDKVFFASVRSGSSQVYFMTLGRISLL	513
1124	TGHLDGVMHKRAQRLKFLCERNDKVFFASVRSGSSQVYFMTLGRISLL	1173
	514 SW 515	
	1174 SW 1175	

FIG. 43 (CONT.¹)

```

64  LTANETQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CD 113
   | ::::::::::::::::::::::::::::::::::::::::::::::::::::
771 LIVRQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CD 820

114 GMRPEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAAL 163
   |::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
821 GMRPEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAAL 870

164 WGVNLLVGTEGMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLTISG 213
   |::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
871 WGVNLLVGTEGMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLTISG 920

214 KKDCLRYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERI 263
   |::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
921 KKDCLRYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERI 970

264 KFLVIALKSSVEVYAWAPKPYHKFMFKSFGELVHKPPLLVDLTVEEGQRL 313
   |::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
971 KFLVIALKSSVEVYAWAPKPYHKFMFKSFGELVHKPPLLVDLTVEEGQRL 1020

```

FIG. 44

314	KVIYGSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELL	363
1021	KVIYGSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELL	1070
364	VCYEDEGVYVNTYGRITKDVVLQWGE MPTSVAYIRSNQTMGWGEKAIEIR	413
1071	VCYEDEGVYVNTYGRITKDVVLQWGE MPTSVAYIRSNQTMGWGEKAIEIR	1120
414	SVETGHL DGVFMHKRAQRLKFLCERN DKVFFASVRS GGSSQVYFMTLGR T	463
1121	SVETGHL DGVFMHKRAQRLKFLCERN DKVFFASVRS GGSSQVYFMTLGR T	1170
	464 SLLSW	468
	1171 SLLSW	1175

FIG. 44 (CONT.¹)

```

1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50
  |||||
1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50

51 GWEIISGVDEHYTPIRTYQVCNVMDHSDQNNWLRTNWVPRNSAQKIYVELK 100
  |||||
51 GWEIISGVDEHYTPIRTYQVCNVMDHSDQNNWLRTNWVPRNSAQKIYVELK 100

101 FTLRDCNSIPLVLGTCKETFNLYMESDDDHGVKFRHQFTKIDTIAADE 150
  |||||
101 FTLRDCNSIPLVLGTCKETFNLYMESDDDHGVKFRHQFTKIDTIAADE 150

151 SFTQMDLGDRIKLNTEIREVGPVNKKGFYLAQDVGACVALSVRVYFK 200
  |||||
151 SFTQMDLGDRIKLNTEIREVGPVNKKGFYLAQDVGACVALSVRVYFK 200

201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNNSKEEDPPRMYCSTEGEW 250
  |||||
201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNNSKEEDPPRMYCSTEGEW 250
    
```

FIG. 45

FIG. 45 (CONT.¹)

[illegible]

FIG. 45 (CONT.)²

FIG. 46

FIG. 46 (CONT.¹)

```

1 MEVVDPPQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIGKYL 50
  |||||
1 MEVVDPPQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIGKYL 50
  . . .
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  . . .
101 LLRRLRHKNVIQLVVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFV 150
  |||||
101 LLRRLRHKNVIQLVVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFV 150

151 CQAHG 155
   |||||
151 CQAHG 155

```

FIG. 47

```

1 MEVDPQQLGMFTEGELMSGMDTFIHRIDSTEVYQPRRKRAKLIKYL 50
  |||||
1 MEVDPQQLGMFTEGELMSGMDTFIHRIDSTEVYQPRRKRAKLIKYL 50

51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100

101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFVP 150
  |||||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFVP 150

151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIKPGNLLLTGGTLKISDLGVAE 199
  |||||
151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIKPGNLLLTGGTLKISDLGVAE 199

```

FIG. 48

27 VKDFLSQLRSSNRRFSIPESGQGGTMDGFRRTIENQHSRNDVMVSEWLN 76
|||||:|||||
301 VKDFLSQLKSSNRRFSIPESGQGGTMDGFRRTIENQHSRNDVMVSEWLN 350
77 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 126
|||||
351 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 400
127 TSTFRNQMPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 176
|||||
401 TSTFRNQMPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 450
177 NIYNCSGVQVGDNNYLTMQTTALPTWGLAPSGKGRGLQHPPVGSQEGP 226
|||||
451 NIYNCSGVQVGDNNYLTMQTTALPTWGLAPSGKGRGLQHPPVGSQEGP 500
227 KDPEAWSRPQGWYNHSGK 244
|||||
501 KDPEAWSRPQGWYNHSGK 518

FIG. 49

FIG. 50

1	MRLTL	CCTW	REERM	GEEG	SELP	V	C	A	S	C	G	Q	R	I	Y	D	G	Q	Y	L	Q	A	L	N	A	D	W	H	A	D	C	F	50										
1	MRLTL	CCTW	REERM	GEEG	SELP	V	C	A	S	C	G	Q	R	I	Y	D	G	Q	Y	L	Q	A	L	N	A	D	W	H	A	D	C	F	50										
51	RCCDC	SASL	SHQY	EKDG	QLF	C	K	K	D	Y	W	A	R	Y	G	E	S	C	H	G	C	S	E	Q	I	T	K	L	V	M	V	A	G	100									
51	RCCDC	SASL	SHQY	EKDG	QLF	C	K	K	D	Y	W	A	R	Y	G	E	S	C	H	G	C	S	E	Q	I	T	K	L	V	M	V	A	G	100									
101	ELKYH	PECF	ICLT	CGTF	I	G	D	G	D	T	Y	T	L	V	E	H	S	K	L	Y	C	G	H	C	Y	Q	T	V	V	T	P	V	I	E	Q	I	150						
101	ELKYH	PECF	ICLT	CGTF	I	G	D	G	D	T	Y	T	L	V	E	H	S	K	L	Y	C	G	H	C	Y	Q	T	V	V	T	P	V	I	E	Q	I	150						
151	LPDSP	GS	HLPH	T	V	T	L	V	S	I	P	A	S	S	H	G	K	R	G	L	S	V	I	D	P	P	H	G	P	P	C	G	T	E	H	S	H	T	V	R	200		
151	LPDSP	GS	HLPH	T	V	T	L	V	S	I	P	A	S	S	H	G	K	R	G	L	S	V	I	D	P	P	H	G	P	P	C	G	T	E	H	S	H	T	V	R	200		
201	VQGVDP	GC	MS	P	D	V	K	N	S	I	H	V	G	D	R	I	E	I	N	G	T	P	I	R	N	V	P	L	D	E	I	D	L	L	I	Q	E	T	S	R	L	L	250
201	VQGVDP	GC	MS	P	D	V	K	N	S	I	H	V	G	D	R	I	E	I	N	G	T	P	I	R	N	V	P	L	D	E	I	D	L	L	I	Q	E	T	S	R	L	L	250

FIG. 51


```

251 QLTLEHDPHDTLGHGLPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
    |||||
251 QLTLEHDPHDTLGHGLPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
    |||||

301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGCF 350
    |||||
301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGCF 350

351 GQAIKV 356
    |||||
351 GQAIKV 356

```

FIG. 51 (CONT.¹)

```

      . . . . .
1  MRLTLCCTWREERMGEELPVCASCGQRIYDGQYLQALNADWHADCF 50
      |||||
1  MRLTLCCTWREERMGEELPVCASCGQRIYDGQYLQALNADWHADCF 50

      . . . . .
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
      |||||
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

      . . . . .
101 ELKYHPECFICLTGTFIGDGTITLVEHSKLYCGHCYYQTVVTPVIEQI 150
      |||||
101 ELKYHPECFICLTGTFIGDGTITLVEHSKLYCGHCYYQTVVTPVIEQI 150

      . . . . .
151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCCGTEHSHTVR 200
      |||||
151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCCGTEHSHTVR 200

      . . . . .
201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
      |||||
201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51

```

251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVLRSCSID 300

301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350
|||||
301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350

```

```
351 GQAIKV 356
      |||||
351 GQAIKV 356
```

FIG. 51 (CONT.¹)

[illegible]

FIG. 52

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FIG. 52 (CONT.¹)

1	MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL	50
1	MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL	50
51	KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHQQQLQELHAHVVL	100
51	KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHQQQLQELHAHVVL	100
101	PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVQKQGAENMIQ	150
101	PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVQKQGAENMIQ	150
151	TYSNGSTKDRKLLLLTAQQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD	200
151	TYSNGSTKDRKLLLLTAQQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD	200
201	DTQGSPDLGAVELRIEELRHFFRVEHAEGAENLRLLSAAKAPDRKAV	250
201	DTQGSPDLGAVELRIEELRHFFRVEHAEGAENLRLLSAAKAPDRKAV	250

FIG. 53

251	SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF	300
251	SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF	300
301	STRLAGPFFPATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG	350
301	STRLAGPFFPATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG	350
351	PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT	400
351	PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT	400
401	VVGQTSWKPCGPNAWDQSFTLELERARELELAVFWRDQRGLCALKFLKLE	450
401	VVGQTSWKPCGPNAWDQSFTLELERARELELAVFWRDQRGLCALKFLKLE	450
451	DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQCK	500
451	DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQCK	500

FIG. 53 (CONT.¹)

FIG. 53 (CONT.²)

FIG. 53 (CONT.²)


```

      . . . . . 723
723 ..... 723
      . . . . . 800
751 EGYVKIADFGLCKEGMGYDRTSTFCGTPEFLAPEVLTDTSYTRAVDWWG 800
      . . . . . 723
723 ..... 723
      . . . . . 850
801 LGVLLYEMLVGESPFPGDDDEEVFDSIVNDEVRYPRFLSAEAI GIMRRLL 850
      . . . . . 738
724 .....RLPPPFPVPTLSGRTD 738
      | | | | | | | | | |
851 RRNPERRLGSSERDAEDVKKQPFRTLGWEALLARRLPPFPVPTLSGRTD 900
      . . . . . 780
739 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDFVAGGC 780
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
901 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDFVAGGC 942

```

FIG. 53 (CONT.³)

```

1 MASDAVQSEPRSWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50
  |||||
1 MASDAVQSEPRSWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50

.
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100
  |||||
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100

.
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150
  |||||
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150

.
151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
  |||||
151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200

.
201 DTQGSDDLGAVELRIEELRHHFRVEHVAEAGAKNVLRLLSAAKAPDRKAV 250
  |||||
201 DTQGSDDLGAVELRIEELRHHFRVEHVAEAGAKNVLRLLSAAKAPDRKAV 250

```

FIG. 54

251	SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF	300
251	SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF	300
301	STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG	350
301	STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG	350
351	PGTPDSRPPFLSRPARGLYSRSGSLGRSSLKAEAEANTSEVSTVLKLDNT	400
351	PGTPDSRPPFLSRPARGLYSRSGSLGRSSLKAEAEANTSEVSTVLKLDNT	400

FIG. 54 (CONT.)¹

FIG. 55

```

90 LSGASFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRRLVKDP 139
   |||||
211 LSGASFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRRLVKDP 260
   |||||

140 KRRMTIAQSLEHSWIKAIRRRRNVRGSDSGRKPERRRLLKTTRLKEYTIKSH 189
   |||||
261 KRRMTIAQSLEHSWIKAIRRRRNVRGSDSGRKPERRRLLKTTRLKEYTIKSH 310
   |||||

190 SSLPPNNSYADFERFSKVLEEAAAEEGLRELQRSRRILCHEDVEALAAIY 239
   |||||
311 SSLPPNNSYADFERFSKVLEEAAAEEGLRELQRSRRILCHEDVEALAAIY 360
   |||||

240 EEKEAWYREESDSLGGDLRRLRQEILLKTEALKRQAQEEAKGALLGTSGLK 289
   |||||
361 EEKEAWYREESDSLGGDLRRLRQEILLKTEALKRQAQEEAKGALLGTSGLK 410
   |||||

290 RRFSLERNRYEALAKQVASEMRFFVQDLVRALEQEKLQGVECGLR 333
   |||||
411 RRFSLERNRYEALAKQVASEMRFFVQDLVRALEQEKLQGVECGLR 454

```

FIG. 56

```

61  GETALHKAACQNRNRAVCQLLVDAGASLRKTD SKGKTPQERAQQAGDPDLA 110
    |||||
995 GETALHKAACQNRNRAVCQLLVDAGASLRKTD SKGKTPQERAQQAGDPDLA 1044
    .
    111 AYLESRQNYKVIGHEDLETAV 131
    |||||
    1045 AYLESRQNYKVIGHEDLETAV 1065
  
```

FIG. 57

```

1 MRGAARLGRPGRSCLPGPALRAPRPPPLLLLALLPLLPAGAAAAPAPR 50
  |||||
1 MRGAARLGRPGRSCLPGPALRAAAP..ALLARCAVAAAAGLRAAARPR 48
  |||||

51 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFSLL 100
  |||||
49 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFNLL 98
  |||||

101 VPSETNFLHFTWHAKSKVEYKLGQVDNVLAMDMPQVNISVQGEVPRTLS 150
  |||||
99 VPSETNFLHFTWHAKSKVEYKLGQVDNVLAMDMPQVNISVQGEVPRTLS 148
  |||||

151 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMKYKKLEEV 200
  |||||
149 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMKYKKLEEV 198
  |||||

201 KTSALDKNTSRTIYDPVHAAPTSTTRVFYISVGVCCAVIFLVAIILAVLH 250
  |||||
199 KTSALDKNTSRTIYDPVHAAPTSTTRVFYISVGVCCAVIFLVAIILAVLH 248
  |||||

251 LHSMKRIELDD 261
  ||:|||||
249 LHNMKRIELDD 259

```

FIG. 58

```

1  MPQVNI SVQGEVPRTL SVFRVELSCTGKVDSEVMILMQNLNTVNSSKNFT 50
   |||||
132 MPQVNI SVQGEVPRTL SVFRVELSCTGKVDSEVMILMQNLNTVNSSKNFT 181
   .
51  VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTTSTRVFI SVG 100
   |||||
182 VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTTSTRVFI SVG 231
   .
101 VCCAVIFLVAII LAVLHLHSMKRIELDDSI SASSSSQGLSQPSTQTQYL 150
   |||||
232 VCCAVIFLVAII LAVLHLHNMKRIELDDSI SASSSSQGLSQPSTQTQYL 281
   .
151 RADTPNNATPITSSYYPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 200
   |||||
282 RADTPNNATPITS..YPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 329
   .
201 KDV LQEGTFGRIFHGILIDEKDPNKEKQAFVKT VKDQASEIQVTMMLTES 250
   |||||
330 KDV LQEGTFGRIFHGILIDEKDPNKEKQAFVKT VKDQASEIQVTMMLTES 379

```

FIG. 59


```

1  MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 50
    |||||||
484 MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 533
    .
51  PSPRATDPPSHL.....DGPPAVAVGQCPLVGP.GPMHRRHL 86
    |||||||:
534 PSPRATDPPSHMAPRPWLWASARWGWQAPCTAATCCSLPGSLGLAYRR.. 581
    .
87  LLPARVP...RPGLEALSLLFAVVLRSAAALGCIGLVAHAGQLTAVWR 133
    | | | | |
582 .....RFPCSCSP.....LFCLVPPPPWAALGWWTPTPANSFQ..... 612
    .
134 RPGAARAP 141
    |||: |
613 .SGAAQEP 619
    
```

FIG. 60

```

1  MELQAEGATAVTGVSPRATDPPSHL.....DGPPAVAVGQ 37
   |||||
519 MELQAEGATAVTGVSPRATDPPSHMAPRPWLWASARWGWQAPCTAATC 568
      |||||
38  CPLVGP.GPMHRRHLLPARVP...RPGLSEALSLLFAVVLSRAAALGC 83
   ||| | | :|| | | | | ||::| ||||
569 CSLPGSLGLAYRR.....RFPCSCSP.....LFCLVPPPPWAALGW 603
      .
      84  IGLVAHAGQLTAVWRRRPGAARAP 106
          |::| | |||: |
      604 WPTPANSPQ.....SGAAQEP 619

```

FIG. 61

```

6  HEDFEFISGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA  50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
580 HEDFEFIFILGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA  624

```

FIG. 62

FIG. 63

```
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDDVDLPYP 50
  |||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDDVDLPYP 50
  |||||
51 LNNFSVASSVMFR 63
  |||||: :::
51 LNNFSVAKCQLMK 63
```

FIG. 64

1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDVLDLPY 50
|||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDVLDLPY 50
51 LNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPPEEREETE 100
|||||
51 LNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPPEEREETE 100
101 AIQAVADRLQRQEEERMNCSPSTQIDNIGEEEMDASTTHHKRKTMNDFDY 150
|||||
101 AIQAVADRLQRQEEERMNCSPSTQIDNIGEEEMDASTTHHKRKTMNDFDY 150
151 LKLLGKGTFGKVILVREKASGYAMKILKKEVIAK 187
|||||
151 LKLLGKGTFGKVILVREKASGYAMKILKKEVIAK 187

FIG. 65

```

73 SSQYDERCFMFLISPTKSVIITILSLFTLQLFFHLSRERVFSEDRTR 122
   | | | : | | ::      : ||||| ||||| ||||| |||||
214 SFQTKDRLCFVMEYVNGG.....ELFFHLSRERVFSEDRTR 249

123 FYGAIEVSALDYLHSGKIVYRDCLKLENMLDKDGHIKITDFGLCKEGITD 172
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 FYGAIEVSALDYLHSGKIVYRDCLKLENMLDKDGHIKITDFGLCKEGITD 299

173 AATMKTFCGTPEYLAPLEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQ 222
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 AATMKTFCGTPEYLAPLEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQ 349

223 DHEKLFEILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGGPDDAKEI 272
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 DHEKLFEILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGGPDDAKEI 399

273 MRHSFFSGVNWQDVYDKKLVPFPKPQVTSETDTRYFDEEFTAQTITITPP 322
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 MRHSFFSGVNWQDVYDKKLVPFPKPQVTSETDTRYFDEEFTAQTITITPP 449

          .
        323 EKYDEDGMDCMDNERRPHPFPQFSYSASGRE 352
           ||||| ||||| ||||| ||||| ||||| |||||
        450 EKYDEDGMDCMDNERRPHPFPQFSYSASGRE 479

```

FIG. 66


```

1  MELLRTITYQPAASTKMCEQALGKCGGNSKKRPPQPPFESQPPQSQAQ  50
  |||||||
1  MELLRTITYQPAASTKMCEQALGKCGGDSKKRPPQPPFESQPPQSQAQ  50
  |||||||
51 VPAAAPHHHHHSHSGPEISRIIVDPPTTGKRYCRGKVLGKGGFACCYEMT  100
  |||||||
51 VPAAAPHHHHHSHSGPEISRIIVDPPTTGKRYCRGKVLGKGGFACCYEMT  100
  |||||||
      . . .
      101 DLTNNKVYAAKIIPHRSRVAKPHQREKVCMTLE  132
      |||||||
      101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIE  132

```

FIG. 67

```

1 MELLRTITYQPAASTKMCEQALGKGCGGNSKKRPPQPPESQPPQSQAQ 50
  |||||
1 MELLRTITYQPAASTKMCEQALGKGCGGDSKKRPPQPPESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYSRR..VSVNSYLRTFAYPELTWYSKSI LSGI 191
  |||||
151 DKENIYILLEYSRRSMAHILKARKVLTEPEVRYLRQIVSGL 193

```

FIG. 68

```

1 MELLRTITYQPAASTKMCEQALGKCGGNSKKRPPQPPEESQPPQSQAQ 50
  |||||
1 MELLRTITYQPAASTKMCEQALGKCGGDSKKRPPQPPEESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYSRR 165
  |||||
151 DKENIYILLEYSRR 165

```

FIG. 69

```

1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50
  |||||
1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50

51 ILCHEQQDREEAQREADMHRLFNHPNIIRLVAYCLRERGAKHEAWLLLPF 100
  |||||
51 ILCHEQQDREEAQREADMHRLFNHPNIIRLVAYCLRERGAKHEAWLLLPF 100

```

101 FK 102

101 FK 102

FIG. 70

1 MERAI SPGLLV RALL LLLL GLAARTVAAGRARGLPAPTAAEAFGLGAAA 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MERAI SPGLLV RALL LLLL GLAARTVAAGRARGLPAPTAAEAFGLGAAA 50

51 APTSATRVPAAGAVAAAEVTVEDAEALPAAAGEQEPRGPEPDDETELPR 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 APTSATRVPAAGAVAAAEVTVEDAEALPAAAGEQEPRGPEPDDETELPR 100

101 GRSLV IISTLDGR IAALDPENHGKKQWDLVDGSGSLVSSLSKPEVFGNK 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 GRSLV IISTLDGR IAALDPENHGKKQWDLVDGSGSLVSSLSKPEVFGNK 150

151 MIIPSLDGA LFQWRDRDRESMETVPFTVESLLESSYKFGGDDVVLVGGSILT 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 MIIPSLDGA LFQWRDRDRESMETVPFTVESLLESSYKFGGDDVVLVGGSILT 200

FIG. 71

```

201 TYGLSAYSGKVRYICSALGCRQWSDEMEQQEEDILLQRTQKTVRavgpr 250
|||||
201 TYGLSAYSGKVRYICSALGCRQWSDEMEQQEEDILLQRTQKTVRavgpr 250

251 SGNEKWNFSVGHFELRYIPDMETRAGFIESTFKPNENTEEskiiSDVEEQ 300
|||||
251 SGNEKWNFSVGHFELRYIPDMETRAGFIESTFKPNENTEEskiiSDVEEQ 300

301 EAAIMDIVIKVSADWKVMFAFSKKGHLEWEYQFCTPIASAWLLKDGKVI 350
|||||
301 EAAIMDIVIKVSADWKVMFAFSKKGHLEWEYQFCTPIASAWLLKDGKVI 350

351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
|||||
351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400

401 RISEKFPSSPKALESVTNENAIIPLTIKWKPLIHSPSRTPVLVGSDEFD 450
|||||
401 RISEKFPSSPKALESVTNENAIIPLTIKWKPLIHSPSRTPVLVGSDEFD 450

```

FIG. 71 (CONT.¹)

451 KCLSNDFSHSEYSNGALSILQYPYDNGYLYLPYKRNKRSTQITVRFL 500
|||||
451 KCLSNDFSHSEYSNGALSILQYPYDNGYLYLPYKRNKRSTQITVRFL 500
501 DNPYNNKIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
|||||
501 DNPYNNKIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
551 RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR 600
|||||
551 RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR 600
601 GGFGVVF EAKNKVDDCN YAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
|||||
601 GGFGVVF EAKNKVDDCN YAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
651 VRYFNAWLEAPPEKWQEKMD EIW LKDESTDWPLSSPSPMDAPSVKIRRM D 700
|||||
651 VRYFNAWLEAPPEKWQEKMD EIW LKDESTDWPLSSPSPMDAPSVKIRRM D 700

FIG. 71 (CONT.²)

FIG. 71 (CONT.³)

FIG. 72

210 210
251 VVLTTPPMKMVTEIAPLGSLDLRLRKHQGHFLGLTSRYAVQVAEGMGYLE 300
210 210
301 SKRFIHRDLAARNLLLATRDLVKIGDFGLMRALPQNDHYYVMQEHKVPF 350
210 210
351 AWCAPESLKTRTFSHASDTWMFGVTLWEMFTYGQEPWIGLNGSQILHKID 400
210 210
401 KEGERLPRPEDCPQDIYNVMVQCWAHKPEDRPTFVALRDFLLEAQPTDMR 450
.....

FIG. 72 (CONT.¹)

```

210 ..... 210
451 ALQDFEFPDKLHIQMNDVITVIEGRAENYWWRGQNTRTLVCVPFRNVVT 500
      .
      .
      .
210 ..... 210
210 ..... 550
501 SVAGLSAQDISQPLQNSFIHTGHGSDSDPRHCWGFPDRIDELYLGNPMDPP 550
      .
      .
      .
211 ..... PPQPAFFTQKPTYDPVSEDQDPLSSDFKRLGLRKPGGLPR 249
      ||| ::|||
551 DLLSVELSTSRPPQHLGGVKKPTYDPVSEDQDPLSSDFKRLGLRKPGGLPR 600
      .
      .
      .
250 GLWLAKPSARVPGTKASRGSGAEVTLIDFGEEPVPALRPCAPSLAQLAM 299
      |||
601 GLWLAKPSARVPGTKASRGSGAEVTLIDFGEEPVP...PYGPAALPGAA 647
      .
      .
      .
300 DACSL..DETPPQSPTRALPRPLHPTPVVDWDARPLPPPAYDDVAQDE 347
      || :| ::| :|||
648 GHGRLLPAGRDPASEPHAGTARPLHPTPVVDWDARPLPPPAYDDVAQDE 697

```

FIG. 72 (CONT.²)

FIG. 72 (CONT.³)

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FIG. 72 (CONT.⁴)

FIG. 73

```

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCDILENVPGRSK 350
|||||
301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCDILENVPGRSK 350

. . . . .
351 ATSVALPGWSPSETRSFMSRTSKSKGSSRNLLKTDDLSDNDVCAVLKLD 400
|||||
351 ATSVALPGWSPSETRSFMSRTSKSKGSSRNLLKTDDLSDNDVCAVLKLD 400

. . . . .
401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
|||||
401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450

. . . . .
451 LEDFLDNQRHGMCLYLEPQGTLEFAEVTFFNPVIERRPKLQRQKKIFSKQ 500
|||||
451 LEDFLDNQRHGMCLYLEPQGTLEFAEVTFFNPVIERRPKLQRQKKIFSKQ 500

. . . . .
501 GKTFRLAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
|||||
501 GKTFRLAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550

551 IPQLAPPA 558
|||||
551 IPQLAPPA 558

```

FIG. 73 (CONT.¹)

```

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLDFSDTMVQKLDIDK 50
  |||
1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLDFSDTMVQKLDIDK 50

. . .
51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100
  |||
51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100

. . .
101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRLKALQKQLDIELK 150
  |||
101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRLKALQKQLDIELK 150

. . .
151 VKQGAENMIQYNSGSSKDRKLHGTAQQLQDSKTKIEVIRMQILQAVQT 200
  |||
151 VKQGAENMIQYNSGSSKDRKLHGTAQQLQDSKTKIEVIRMQILQAVQT 200

. . .
201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250
  |||
201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250

```

FIG. 74

251	RKALSEAQA	RNFNESSQ	KLDLLKYS	LEQRLNE	VPKNHPK	SRIIEE	LSLVA	300
251	RKALSEAQA	RNFNESSQ	KLDLLKYS	LEQRLNE	VPKNHPK	SRIIEE	LSLVA	300
301	ASPTLSPRQ	SMISTQNQ	YSTLSKPA	ALTGTLE	VRMLGCQ	DILEN	VPGRSK	350
301	ASPTLSPRQ	SMISTQNQ	YSTLSKPA	ALTGTLE	VRMLGCQ	DILEN	VPGRSK	350
351	ATSVALPG	WSPSETR	SSFMSTR	SKSKSG	SSRNLLK	TDDL	SNDCAVL	400
351	ATSVALPG	WSPSETR	SSFMSTR	SKSKSG	SSRNLLK	TDDL	SNDCAVL	400
401	NTVVGQTS	WKPI	SNQSWDQ	KFTLE	DRSRE	LEISVY	WRDWSL	450
401	NTVVGQTS	WKPI	SNQSWDQ	KFTLE	DRSRE	LEISVY	WRDWSL	450

FIG. 74 (CONT.¹)

451	LEDFLDNQRHGMCLYLEPQGT	FAEVTFFNPVIERRPKLQRQKKI	FSKQQ	500
451	LEDFLDNQRHGMCLYLEPQGT	FAEVTFFNPVIERRPKLQRQKKI	FSKQQ	500
501	GKTFLRAPQMNINIA	TWGRLVRRRAIPTVNHSGTFSPQAPV	TTVPVVDVR	550
501	GKTFLRAPQMNINIA	TWGRLVRRRAIPTVNHSGTFSPQAPV	TTVPVVDVR	550
551	IPQLAPPASDSTVT	TKLDFDLEPEPPAPP	RASSLGEIDESSEL	RVL
551	IPQLAPPASDSTVT	TKLDFDLEPEPPAPP	RASSLGEIDESSEL	RVL
601	QAS	603		
601	QDS	603		

FIG. 74 (CONT.²)

```

1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50
  |||||
1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50

51 TSELLGEGAYAKVQGA VSLQNGKEYAVKI IEKQAGHSRVRFREVE TLYQ 100
  |||||
51 TSELLGEGAYAKVQGA VSLQNGKEYAVKI IEKQAGHSRVRFREVE TLYQ 100

101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGT 131
  |||||
101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGG 131
    
```

FIG. 75

FIG. 76

```

1  MSGMKLNNSCTPIITPELTTPCGSAEYMAPEVVEFTDQATFYDKRCDL 50
   :|||||||||||||||||||||||||||||||||||||||||
194 LGSGMKLNNSCTPIITPELTTPCGSAEYMAPEVVEFTDQATFYDKRCDL 243

   . . . . .
51  WSLGVVLYIMLSGYPPFVGHCGADCGWDRGEVCRVCQNKLFESIQEGKYE 100
   |||||||||||||||||||||||||||||||||||||||
244 WSLGVVLYIMLSGYPPFVGHCGADCGWDRGEVCRVCQNKLFESIQEGKYE 293

   . . . . .
101 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 150
   |||||||||||||||||||||||||||||||||||||||
294 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 343

   . . . . .
151 TPQVLQRNSSTMDLTTLFAAEAIALNRQLSQHEENELAEFPEALADGLCSM 200
   |||||||||||||||||||||||||||||||||||||||
344 TPQVLQRNSSTMDLTTLFAAEAIALNRQLSQHEENELAEFPEALADGLCSM 393

   . . . . .
201 KLSPPCKSRLARRRALAQAGGEDRSPPTAL 231
   |||||||||||||||||||||||||||||||
394 KLSPPCKSRLARRRALAQAGGEDRSPPTAL 424

```

FIG. 77

```

1 MRKGVVKDPEIADLFYKDDPEELFIGLHEIGHGSGFGAVYFATNAHTSEV 50
  |||||
1 MRKGVVKDPEIADLFYKDDPEELFIGLHEIGHGSGFGAVYFATNAHTSEV 50

51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100

101 MEYCLGSASDLLLEVHKKPLQVEIAAITHGALHGLAYLHSHALIHR 146
   |||||
101 MEYCLGSASDLLLEVHKKPLQVEIAAITHGALHGLAYLHSHALIHR 146

```

FIG. 78

```

2 MEELHSLDPRRQELLEARFTGVGVSKGPLNSESSNQSLCSVGLSDKEVE 51
  |||||
1 MEELHSLDPRRQELLEARFTGVGVSKGPLNSESSNQSLCSVGLSDKEVE 50
  |||||
52 TPEKKQNDQNRNRKKAEPYETSQKGKGTPRGHKISDYFETA 91
  |||||
51 TPEKKQNDQNRNRKKAEPYETSQKGKGTPRGHKISDYFEFA 90
  |||||

```

FIG. 79

```

27 KDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 76
   |||||
435 KDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 484

77 CHLSWAWASWPAAACTAGPKGRPPMTQVYERLEKLAQAVVAGVPGHLEA 126
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
485 CPPELGLGLGQLACCCCLHRRRAKRRPPMTQVYERLEKLAQAVVAGVPGHLEA 534

127 ASCI.PFPQENSYSVSTGRAHSGAAPWQPLAAPSGASAAQAAEQLRGPNQ 175
   |||| | |||||
535 ASCIPSPQENSYSVSTGRAHSGAAPWQPLAAPSGASAAQAAEQLRGPNQ 584

176 PVESDESLGGLSAAALRSWHLTPSCPLDPAPLREAGCPQGDTAGESSWGSG 225
   |||||
585 PVESDESLGGLSAAALRSWHLTPSCPLDPAPLREAGCPQGDTAGESSWGSG 634

226 PGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSL 275
   |||||
635 PGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSL 684

276 QLLSSSSSLPGLGLEQDRQGPKKVMNFRA 303
   |||||
685 QLLSSSSSLPGLGLEQDRQGPEESDEFQS 712

```

FIG. 80

20 QTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL 69
 |||||
 303 QTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL 352

 70 TPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLA 119
 |||||
 353 TPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLA 402

 120 VDTDTSFGVVVLETLAQORAVKTHGARTKYLKDLVEEEAEEAGVALRST 169
 |||||
 403 VDTDTSFGVVVLETLAQORAVKTHGARTKYLKDLVEEEAEEAGVALRST 452

 170 QSTLQAGLAADAWAAPIAMQIYKKHLDPGPGCHLSWAWAWASWPAAACT 219
 | ||||| : : : : :
 453 QSTLQAGLAADAWAAPIAMQIYKKHLDPGPGCPPELGLGLGQLACCLH 502

 220 AGPKGRPPMTQVYERLEKLQAVVAGVPGHLEAASCI.PFPQENSYSVSSTG 268
 | |||||
 503 RRAKRRPPMTQVYERLEKLQAVVAGVPGHLEAASCIPPSPQENSYSVSSTG 552

FIG. 81

```
269 RAHSGAAPWQPLAAPSGASAAEQIQRGNQPVESDESLGGLSAAALRSW 318
|||||
553 RAHSGAAPWQPLAAPSGASAAEQIQRGNQPVESDESLGGLSAAALRSW 602

319 HLTSCPLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSAS 368
|||||
603 HLTSCPLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSAS 652

369 SSSEPPQIIINPARQKVMQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQ 418
|||||
653 SSSEPPQIIINPARQKVMQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQ 702

419 GPKKVMNFRA 428
||::: ||:::
703 GPEESDEFQS 712
```

FIG. 81 (CONT.¹)

```

1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIV 50
  |||||
1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIV 50
  |||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIIT 100
  |||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIIT 100
  |||||
101 AWHPPAPLPSPGTTAPRPSSIIPAPAEAEAWSPRKLPSSASTFLSPAFFGS 150
  |||||
101 AWHPPAPLPSPGTTAPRPSSIIPAPAEAEAWSPRKLPSSASTFLSPAFFGS 150
  |||||
151 QTHSGPELGLVPSPASLWPPPPSPAPSSSTKPGPESSVSLQGARPSPCFW 200
  |||||
151 QTHSGPELGLVPSPASLWPPPPSPAPSSSTKPGPESSVSLQGARPSPCFW 200
  |||||

```

FIG. 82

```

201 PLCEISRGTNHFSEELKIGEGGFCVYRAVMRNTVYAVKRLKENADLEWT 250
    |||||
201 PLCEISRGTNHFSEELKIGEGGFCVYRAVMRNTVYAVKRLKENADLEWT 250
    |||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
    |||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
    |||||
301 HCQTQACPPLSWPQRLDILLGTARASQVSCNRVSSCVSKSSPGL 344
    |||||
301 HCQTQACPPLSWPQRLDILLGTARAIQF.....LHQDSPSL 336
    |||||

```

FIG. 82 (CONT.¹)

1 MFTEEDVKFYLAELALALDHLHSLGIYRDLKPENILLDEEGHIKLTDFG 50
 |||||
 164 MFTEEDVKFYLAELALALDHLHSLGIYRDLKPENILLDEEGHIKLTDFG 213
 . . .
 51 LSKE SIDHEKKAYSFCGTVEYMAPEV VNR RRGHTQ SADWWSFGVLMFEMLT 100
 |||||
 214 LSKE SIDHEKKAYSFCGTVEYMAPEV VNR RRGHTQ SADWWSFGVLMFEMLT 263
 . . .
 101 GTLPFQGGKDRKETMTMILKAKLGMPPQFLSPEAQSLRLMLFKRNPANRLGA 150
 |||||
 264 GTLPFQGGKDRKETMTMILKAKLGMPPQFLSPEAQSLRLMLFKRNPANRLGA 313
 . . .
 151 GPDGV E E I K R H S F F S T I D W N K L Y R R E I H P P F K P A T G R P E D T F Y F D P E F T A 200
 |||||
 314 GPDGV E E I K R H S F F S T I D W N K L Y R R E I H P P F K P A T G R P E D T F Y F D P E F T A 363
 . . .
 201 K T P K D S P G I P P S A N A H Q L F R G S F V A I T S D D E S Q A M Q T V G V H S I V Q Q L H R 250
 |||||
 364 K T P K D S P G I P P S A N A H Q L F R G S F V A I T S D D E S Q A M Q T V G V H S I V Q Q L H R 413
 . . .
 251 NSIQFTDGYEVKEDIGVGSY SVCKRCIHKATNMEFAVKV 289
 |||||:
 414 NSIQFTDGYEVKEDIGVGSY SVCKRCIHKATNMEFAVKI 452

FIG. 83

FIG. 84

1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGAAAVGEGEEHQLPPPP 50
|||||
1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGAAAVGEGEEHQLPPPP 50
|||||
51 PGSFWNVESAAAPGIGCPAATSSSSATRGSSVGGSRRTTVAYVINEA 100
|||||
51 PGSFWNVESAAAPGIGCPAATSSSSATRGSSVGGSRRTTVAYVINEA 100
|||||
101 SQQLVVAESEALQSLREACETVGATLETLHFGLDFGETTVLDRFYNAD 150
|||||
101 SQQLVVAESEALQSLREACETVGATLETLHFGLDFGETTVLDRFYNAD 150
|||||
151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
|||||
151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
|||||
201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMKGLTELMQPNFELLGPIC 250
|||||
201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMKGLTELMQPNFELLGPIC 250

FIG. 85

FIG. 85 (CONT.¹)FIG. 85 (CONT.¹)

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FIG. 86

68 IGS.....AAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLKMCVN 110
||| |||||
70 IGSQAQGI VCAAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLKMCVN 119
111 HKNII SLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYL 160
|||||
120 HKNII SLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYL 169
161 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM 210
|||||
170 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM 219
211 MTPYVVTRYRAPEVILGMGYKENVDIWSV GCIMGEMVRHKILFPGRDYI 260
|||||
220 MTPYVVTRYRAPEVILGMGYKENVDIWSV GCIMGEMVRHKILFPGRDYI 269
261 DQWNKVIEQLGTPCPEFMKKLQPTVRN YVENRPKYAGLTFPKLFPDSLFP 310
|||||
270 DQWNKVIEQLGTPCPEFMKKLQPTVRN YVENRPKYAGLTFPKLFPDSLFP 319

FIG. 87

$$\begin{array}{ccc} 411 & V\bar{Q}\bar{Q} & 413 \\ & ||| & \\ 420 & V\bar{Q}\bar{Q} & 422 \end{array}$$

FIG. 87 (CONT.¹)

FIG. 8

```

1 MAMTGSTPCSSMSNHTKERVTMTKVTLENFYSNLIAQHEEREMRQKKLEK 50
  |||||
1 MAMTGSTPCSSMSNHTKERVTMTKVTLENFYSNLIAQHEEREMRQKKLEK 50
  |||||
51 VMEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGLEDFFESLKVIGRAF 100
  |||||
51 VMEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGLEDFFESLKVIGRAF 100
  |||||
101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHRAERDILVEADSLWVV 150
  |||||
101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHRAERDILVEADSLWVV 150
  |||||
151 KMFYSFQDKLNLYLIMEFLPGGDMMTLLMKKDTLTTEETQFYIAETVLAI 200
  |||||
151 KMFYSFQDKLNLYLIMEFLPGGDMMTLLMKKDTLTTEETQFYIAETVLAI 200
  |||||
201 DSIHQQLGFHARDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250
  |||||
201 DSIHQQLGFHARDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250

```

FIG. 89

251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFSTVGTPDYIAPEVFMQTGYN 300
|||||
251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFSTVGTPDYIAPEVFMQTGYN 300
|||||
301 KLCDWWSLGVIMYEMMLIG 318
|||||
301 KLCDWWSLGVIMYEMMLIG 318

FIG. 89 (CONT.¹)

```

11 VSGGMLDI IKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDI IKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 192
.
61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVKRKT FVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVKRKT FVGTPCWMA 242
.
111 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 292
.
161 PTLTGVEDKEMMKKYGKSFRLKLLSLCLQKDP SKRPTAAELLKCKFFQKA 210
|||||
293 PTLTGVEDKEMMKKYGKSFRLKLLSLCLQKDP SKRPTAAELLKCKFFQKA 342
.
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDD EMD 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDD EMD 392

```

FIG. 90

261 EKSEEGKAAFSQEKSRVRKEENPEIAVSASTIPEQIQSLSVHDSQGPPNA 310
 ||||| 311 NEDYREASSCAVNLVLRNLSRKELNDIRFEFTPGRDTADGVSQELFSAG 360
 393 EKSEEGKAAFSQEKSRVRKEENPEIAVSASTIPEQIQSLSVHDSQGPPNA 442
 443 NEDYREASSCAVNLVLRNLSRKELNDIRFEFTPGRDTADGVSQELFSAG 492
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 410
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 542

411 QLSVS 415
 |||||
 543 QLSVS 547

FIG. 90 (CONT.¹)


```

11 VSGGMLDIIKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDIIKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 192
.
61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 242
.
111 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLMITLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLMITLQNDP 292
.
161 PTLETGVEDKEMMKYKGSFRKLLSLCLQKDP SKRPTAAELLKCKFFQKA 210
|||||
293 PTLETGVEDKEMMKYKGSFRKLLSLCLQKDP SKRPTAAELLKCKFFQKA 342
.
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 392

```

FIG. 91

```

      .      .      .      .      .      .      .      .      .      .
261 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEIQSLSVHDSQGGPPNA 310
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
393 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEIQSLSVHDSQGGPPNA 442
      .      .      .      .      .      .      .      .      .      .
311 NEDYREASSCAVNLVLRNLSRKELNDIRFEFTPGRDTADGVSQELFSAG 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
443 NEDYREASSCAVNLVLRNLSRKELNDIRFEFTPGRDTADGVSQELFSAG 492
      .      .      .      .      .      .      .      .      .      .
361 LVDGHDVVIIVAANLQKIVDDPKALKTLTFKL 391
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
493 LVDGHDVVIIVAANLQKIVDDPKALKTLTFKL 523

```

FIG. 91 (CONT.¹)